

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/553,305
Source: PU/10
Date Processed by STIC: 10/25/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. **EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
2. **U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/553,305

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleic
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4 Non-ASCII The submitted file was **not saved** in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your **subsequent submission is saved in ASCII text**.

5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules**, each n or Xaa **can only represent** a single residue. Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the **only valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11 Use of <220>
 → Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 Misuse of n/Xaa "n" **can only represent** a single nucleotide; "Xaa" **can only represent** a single amino acid



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/553,305

DATE: 10/25/2005
TIME: 10:08:24

Input Set : A:\sequence_listing.txt
Output Set: N:\CRF4\10252005\J553305.raw

3 <110> APPLICANT: Japan EnviroChemicals, Ltd.
5 <120> TITLE OF INVENTION: A protein binding to plasticizers
7 <130> FILE REFERENCE: 09622
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/553,305
C--> 9 <141> CURRENT FILING DATE: 2005-10-14
9 <150> PRIOR APPLICATION NUMBER: JP 2003-110877
W--> 10 <151> PRIOR FILING DATE: 2003-04-15 2003-04-15 ← use this format for dates
E--> 12 <160> NUMBER OF SEQ ID NOS: 27 34 ← see p. 2
14 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

155 <210> SEQ ID NO: 5 15 shown below
156 <211> LENGTH: 5
157 <212> TYPE: PRT
158 <213> ORGANISM: Artificial
160 <220> FEATURE:
161 <223> OTHER INFORMATION: Linker
163 <400> SEQUENCE: 5
164 Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
E--> 165 1 5 10 15
273 <210> SEQ ID NO: 15
274 <211> LENGTH: 20 36 (p. 2)
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial
278 <220> FEATURE:
279 <223> OTHER INFORMATION: Primer
281 <220> FEATURE:
282 <221> NAME/KEY: misc_feature
283 <222> LOCATION: 24
284 <223> OTHER INFORMATION: i
286 <220> FEATURE:
287 <221> NAME/KEY: misc_feature
288 <222> LOCATION: 25
289 <223> OTHER INFORMATION: i
291 <220> FEATURE:
292 <221> NAME/KEY: misc_feature
293 <222> LOCATION: 29
294 <223> OTHER INFORMATION: i
296 <220> FEATURE:
297 <221> NAME/KEY: misc_feature
298 <222> LOCATION: 30 /

Does Not Comply
Connected Diskette Needed
what is the source of genetic material?
(see item 11 on
Error
summary
sheet)

P.2
Please
correct this
in subsequent
sequences

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/553,305

DATE: 10/25/2005

TIME: 10:08:24

Input Set : A:\sequence_listing.txt
 Output Set: N:\CRF4\10252005\J553305.raw

299 <223> OTHER INFORMATION: i /
 301 <220> FEATURE:
 302 <221> NAME/KEY: misc_feature
 303 <222> LOCATION: 34
 304 <223> OTHER INFORMATION: i /
 306 <220> FEATURE:
 307 <221> NAME/KEY: misc_feature
 308 <222> LOCATION: 35 /
 309 <223> OTHER INFORMATION: i
 311 <400> SEQUENCE: 15
 E--> 312 ggccacgcgt cgactagtagac ggg//nngggnn gggnn//
 612 <210> SEQ ID NO: 34 ← last sequence in submitted file
 613 <211> LENGTH: 66
 614 <212> TYPE: PRT
 615 <213> ORGANISM: Artificial
 617 <220> FEATURE:
 618 <223> OTHER INFORMATION: Primer
 620 <400> SEQUENCE: 34
 621 Gly Gly Gly Gly Ser
 E--> 622 1 5

36

↓
 a primer is not a peptide
 (please give source of genetic material
 as information)

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<210> 10
<211> 18
<212> DNA
<213> Artificial

<400> 10
gcttgccggg tgggccac

Needs explanation
(see p. 4)
for
error explanation

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/25/2005
PATENT APPLICATION: US/10/553,305 TIME: 10:08:25

Input Set : A:\sequence_listing.txt
Output Set: N:\CRF4\10252005\J553305.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#: 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 28, 29, 30, 31, 32, 33, 34

Use of <220> Feature (NEW RULES): *and explanation*

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq# : 10

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/553,305

DATE: 10/25/2005
TIME: 10:08:25

Input Set : A:\sequence_listing.txt
Output Set: N:\CRF4\10252005\J553305.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:10 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:26 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:24
L:99 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:97
L:165 M:252 E: No. of Seq. differs, <211> LENGTH:Input:5 Found:15 SEQ:5
L:226 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial
L:226 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial
L:226 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:226
L:312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:312 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:36 SEQ:15
L:622 M:252 E: No. of Seq. differs, <211> LENGTH:Input:66 Found:5 SEQ:34
L:12 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (27) Counted (34)